

5. US-08-877-150B-36 (1-458)
u49853p_2

Initial Score = 11 Optimized Score = 159 Significance = -0.41
Residue Identity = 16% Matches = 62 Mismatches = 250
Gaps = 42 Conservative Substitutions = 16

60 70 80 90 100 110 120 130
KNRYKDVLPYDQTRVILSLQERGHSDYINGNEIRGVDSGLAVIATQGPLPHTLLDFWRLVWEEGVKVLMA
140 150 160 170 180 190 200
CREIENGRKRCERYAQEQEPLQ-TGLFCITLLIKKWLNEIDIMRLTKVTFKESRSVYQLOQYMSWPDGRVP
110 120 130 140 150 160 170
WRPGTTGRGOSSLVSSATLRPAQWPGLKVCVPLKPAVGLGTTRTATKMXHMMROESSFPCSKRRDMEIT
210 220 230 240 250 260 270
SSPDHMLAMVEARRLQSGGPEPLCV-HCSAGCGRTGVLCVTVDYVQQLLLTQMIIPDFSLFDDVVLKMKRKP
110 120 130 140 150 160 170
SMTSSGAKWEARPTLRRKDP---CLTHCWTSGAWEFGSLGRSXMPVKRQKMDGGSVNATGPGSR-SLXRL
280 290 300 310 320 330
AAVQTEQYRFLYHTVAQMFCSLQNASP-HYONIKENCAPLYDDALFLRT--PQALLAIP-----RPPGGVLR
110 120 130 140 150 160 170
GLSASXQRR---QHXMQ---TSLSGPSRLHRRNSALCTS-YSICPGQTTGPPAVLITFSPPMWRPAAAS-K
340 350 360 370 380 390 400 410
SISVFGSPGHAMADTYAEQKRGAPAGAGSGTGTGTGARSAAEAPLYSKVTPPRAQRGAHAEDARGTLPG
110 120 130 140 150 160 170
GLDLDPVSATVLA--ADEQ-----VSCALLTWXSCCXPROSLPTSVSXKMSWRCNGSLQOCRCORSSTGS
420 430 440 450
RVPA--DQSPAGSAGVAVAGGAGTGGGFGNFRIGRPGKPRDP--p-----AEWTRV
CUTQWLSYSPALSRTPAPTRTSRRATLO-SARKPSGPPQPCPLPHQHGFGFASRCLRPRSPWLTLT
290 300 310 320 330 340 350 360
LMCRSVLRRAQGRGRPPARTPRFTARLHVPSDRW
370 380 390

6. US-08-877-150B-36 (1-458)
u49853p_5

Initial Score = 9 Optimized Score = 114 Significance = -0.42
Residue Identity = 13% Matches = 33 Mismatches = 188
Gaps = 13 Conservative Substitutions = 17

170 180 190 200 210 220 230
KWLNEIDIMRLTKVTFKESRSVYQLOQYMSWPDGRVSPSPDHMLAMVEARRLQSGGPEPLCVHCSAGCGRT
240 250 260 270 280 290 300
GVLCVTVDYVVRQQLLLTQMIIPDFSLFDDVVLKMKRQKPAQVTEQYRFLYHTVAQMFCSLQNASPHYQNIKE
110 120 130 140 150 160 170
TXHTAQOYGGSSPA---TTWQAITGTALVTPVSTLLEDPGALMAFRCAASXSLALQSVLHLLLRHQARK
30 40 50 60 70 80 90
310 320 330 340 350 360 370
NCAPLYDDALFLRTQALLAIPRPFGVLRISVPGSP--GHAMADTYAEQKRGAPAGAGSGTGTGTGT-G
110 120 130 140 150 160 170
SFGPQELGAVPLSPVRP-PCVPPVAGHVEPPGCKSGCPCWMAAPALCPPKRHASAPQRCQPPWGGSGAQ

380 390 400 410 420 430 440
ARSAEEAPLYSKVTPPRAQPG-AHAEDARGTLPGRVPADQSPAG--SGAYEDVAGGA-OTGGLGNLRIGRP
110 120 130 140 150 160
PRCSKEPLLAVAGMMQAGLRRSXGRRLPCR--LERSSPXSGSGGMCWPCGECGRIAEPLCGTGTCTAPLSALLO
170 180 190 200 210 220 230
450 X
KGPRDPPAEWTRV
240 X 250 260 270 280 290
AAVSASGPLGRDXSWEGLSGSAATASHSQORTGHLFVRSQHCSGHRGVQVQALGGSGPPPPW